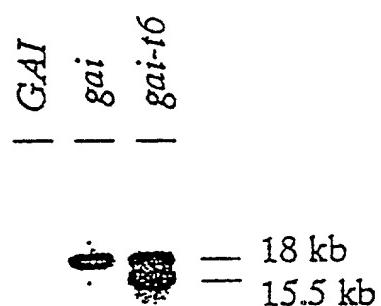
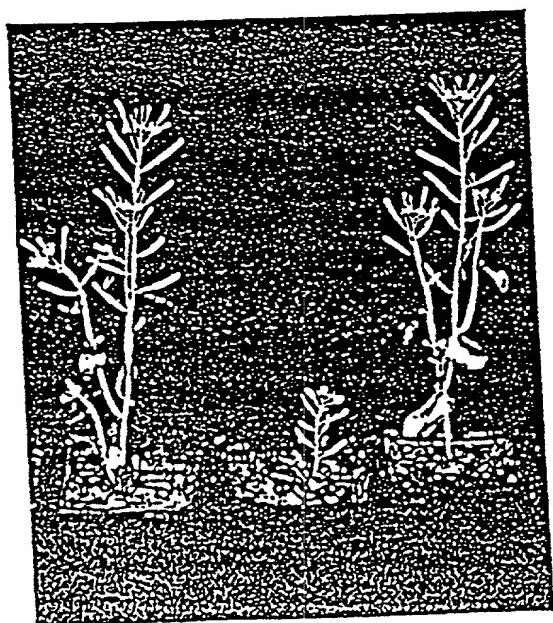
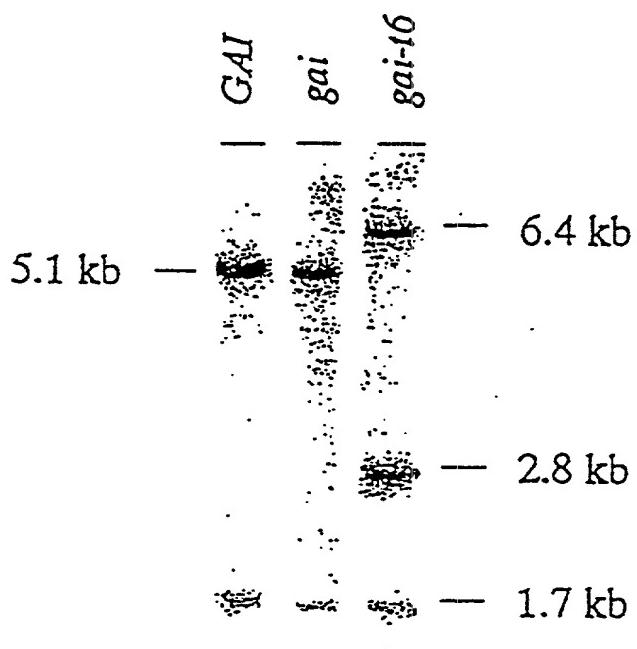


Fig. 1

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Fig. 2 bFig. 2 a

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Fig. 2c

TAATAATCAT	TTTTTTTCTT	ATAACCTTCC	TCTCTATT	TACAATTAT	TTTGGTATTA	60
GAAGTGGTAG	TGGAGTGAAA	AAACAAATCC	TAAGCAGTCC	TAACCGATCC	CCGAAGCTAA	120
AGATTCTTCA	CCTTCCCAA	TAAAGCAAAA	CCTAGATCCG	ACATTGAAGG	AAAAACCTTT	180
TAGATCCATC	TCTGAAAAAA	AACCAACCAT	GAAGAGAGAT	CATCATCATC	ATCATCAAGA	240
TAAGAAGACT	ATGATGATGA	ATGAAGAAGA	CGACGGTAAC	GGCATGGATG	AGCTTCTAGC	300
TGTTCTGGT	TACAAGGTTA	GGTCATCGGA	AATGGCTGAT	GTTGCTCAGA	AACTCGAGCA	360
GCTTGAAGTT	ATGATGTCAT	ATGTCAAGA	AGACGATCTT	TCTCAACTCG	CTACTGAGAC	420
TGTTCACTAT	ATATCCGGCGG	AGCTTTACAC	GTGGCTTGAT	TCTATGCTCA	CCGACCTTAA	480
TCCTCCGTCG	TCTAACGCCG	AGTACGATCT	TAAAGCTATT	CCCGGTGACG	CGATTCTCAA	540
TCAGTTCGCT	ATCGATTCGG	CTTCTTCGTC	TAACCAAGGC	GGCGGAGGAG	ATACGTATAC	600
TACAAACAAG	CGGTTGAAAT	GCTCAAACGG	CGTCGTGAA	ACCAACACAG	CGACGGCTGA	660
GTCAACTCGG	CATGTTGTC	TGGTTGACTC	GCAGGAGAAC	GGTGTGCGTC	TCGTTCACGC	720
GCTTTTGGCT	TGCGCTGAAG	CTGTTCAGAA	GGAGAATCTG	ACTGTGGCGG	AAGCTCTGGT	780
GAAGCAAATC	GGATTCTTAG	CTGTTCTCA	AATCGGAGCT	ATGAGAAAAG	TCGCTACTTA	840
CTTCGCCGAA	GCTCTCGCGC	GGCGGATT	CCGTCTCT	CCGTCGCAGA	GTCCAATCGA	900
CCACTCTCTC	TCCGATACTC	TTCAGATGCA	CTTCTACAG	ACTTGTCCIT	ATCTCAAGTT	960
CGCTCACTTC	ACGGCGAAC	AAGCGATTCT	CGAAGCTTT	CAAGGGAAGA	AAAGAGTTCA	1020
TGTCAATTGAT	TTCTCTATGA	GTCAAGGTCT	TCAATGGCCG	GGCGTTATGC	AGGCTCTTGC	1080
GCTTCGACCT	GGTGGTCC	CTGTTTCCG	GTAAACCGGA	ATTGGTCCAC	CGGCACCGGA	1140
TAATTTCGAT	TATCTTCATG	AAGTGGGTG	TAAGCTGGCT	CATTAGCTG	AGGCGATTCA	1200
CGTTGAGTT	GAGTACAGAG	GATTGTGGC	TAACACTTTA	GCTGATCTTG	ATGCTTCGAT	1260
GCTTGAGCTT	AGACCAAGTG	AGATTGAATC	TGTTGCGTT	AACTCTGTT	TCGAGCTTCA	1320
CAAGCTCTTG	GGACGACCTG	GTGCGATCGA	TAAGGTTCTT	GGTGTGGTG	ATCAGATTAA	1380
ACCGGAGATT	TTCACTGTGG	TTGAGCAGGA	ATCGAACCAT	AATAGTCCGA	TTTCCTTAGA	1440
TCGGTTTACT	GAGTCGTTGC	ATTATTACTC	GACCTTGTT	GACTCGTTGG	AAGGTGTACC	1500
GAGTGGTCAA	GACAAGGTCA	TGTGGAGGT	TTACTTGTT	AAACAGATCT	GCAACGTTGT	1560
GGCTTGTGAT	GGACCTGACC	GAGTTGAGCG	TCATGAAACG	TTGAGTCAGT	GGAGGAACCG	1620
GTTCGGGTCT	GCTGGGTTTG	CGGCTGCACA	TATTGGTTCG	AATGCGTTA	AGCAAGCGAG	1680
TATGCTTTG	GCTCTGTTCA	ACGGCGGTGA	GGGTTATCGG	GTGGAGGAGA	GTGACGGCTG	1740
TCTCATGTTG	GGTTGGCACA	CACGACCGCT	CATAGCCACC	TCGGCTTGG	AACTCTCCAC	1800
CAATTAGATG	GTGGCTCAAT	GAATTGATCT	GTTGAACCGG	TTATGATGAT	AGATTTCCGA	1860
CCGAAGCCAA	ACTAAATCCT	ACTGTTTTTC	CCTTTGTAC	TTGTTAAGAT	CTTATCTTC	1920
ATTATATTAG	GTAATTGAAA	AATTCTAAA	TTACTCACAC	TGGC		1964

MetLysArgAspHisHisHisGlnAspLysLysThrMetMetAsnGluGlu	20
AspAspGlyAsnGly <u>MetAspGluLeuLeuAlaValLeuGlyTyrLysValArgSerSer</u>	40
<u>GluMetAlaAspValAlaGlnLysLeuGluGlnLeuGluValMetMetSerAsnValGln</u>	60
GluAspAspLeuSerGlnLeuAlaThrGluThrValHisTyrAsnProAlaGluLeuTyr	80
ThrTrpLeuAspSerMetLeuThrAspLeuAsnProProSerSerAsnAlaGluTyrAsp	100
LeuLysAlaIleProGlyAspAlaIleLeuAsnGlnPheAlaIleAspSerAlaSerSer	120
SerAsnGlnGlyGlyGlyAspThrTyrThrAsnLysArgLeuLysCysSerAsn	140
GlyValValGluThrThrAlaThrAlaGluSerThrArgHisValValLeuValAsp	160
SerGlnGluAsnGlyValArgLeuValHisAlaLeuLeuAlaCysAlaGluAlaValGln	180
LysGluAsnLeuThrValAlaGluAlaLeuValLysGlnIleGlyPheLeuAlaValSer	200
GlnIleGlyAlaMetArgLysValAlaThrTyrPheAlaGluAlaLeuAlaArgArgIle	220
TyrArgLeuSerProSerGlnSerProIleAspHisSerLeuSerAspThrLeuGlnMet	240
HisPheTyrGluThrCysProTyrLeuLysPheAlaHisPheThrAlaAsnGlnAlaIle	260
LeuGluAlaPheGlnGlyLysLysArgValHisValIleAspPheSerMetSerGlnGly	280
LeuGlnTrpProAlaLeuMetGlnAlaLeuAlaLeuArgProGlyGlyProProValPhe	300
ArgLeuThrGlyIleGlyProProAlaProAspAsnPheAspTyrLeuHisGluValGly	320
CysLysLeuAlaHisLeuAlaGluAlaIleHisValGluPheGluTyrArgGlyPheVal	340
AlaAsnThrLeuAlaAspLeuAspAlaSerMetLeuGluLeuArgProSerGluIleGlu	360
SerValAlaValAsnSerValPheGluLeuHisLysLeuLeuGlyArgProGlyAlaIle	380
AspLysValLeuGlyValValAsnGlnIleLysProGluIlePheThrValValGluGln	400
GluSerAsnHisAsnSerProIlePheLeuAspArgPheThrGluSerLeuHisTyrTyr	420
SerThrLeuPheAspSerLeuGluGlyValProSerGlyGlnAspLysValMetSerGlu	440
ValTyrLeuGlyLysGlnIleCysAsnValValAlaCysAspGlyProAspArgValGlu	460
ArgHisGluThrLeuSerGlnTrpArgAsnArgPheGlySerAlaGlyPheAlaAlaAla	480
HisIleGlySerAsnAlaPheLysGlnAlaSerMetLeuLeuAlaLeuPheAsnGlyGly	500
GluGlyTyrArgValGluGluSerAspGlyCysLeuMetLeuGlyTrpHisThrArgPro	520
LeuIleAlaThrSerAlaTrpLysLeuSerThrAsn	532

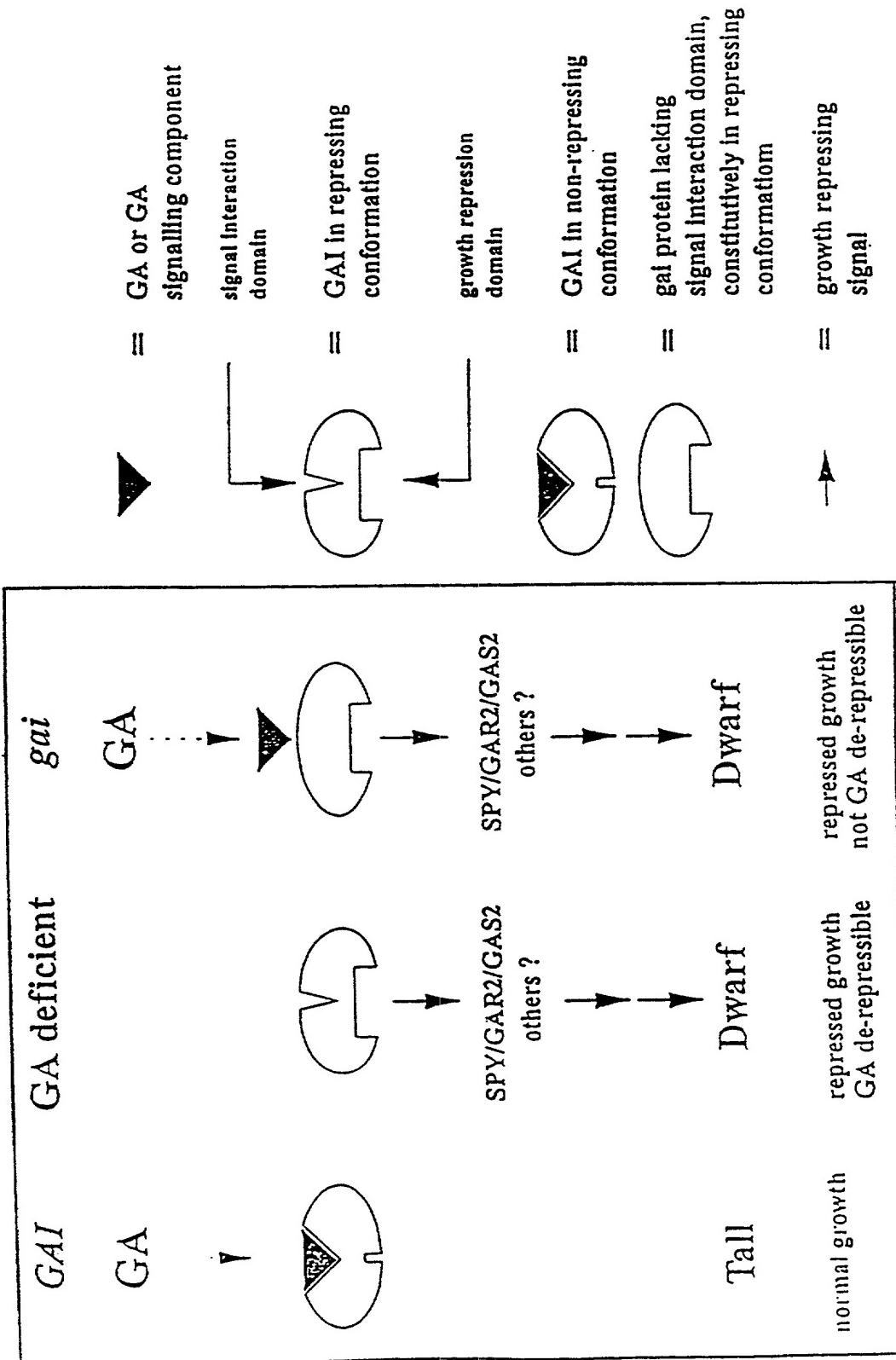


Fig. 5

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Figure 6(a)

1 TAGAAGTGGT AGTGGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
 51 CCCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
 101 CGACATTGAA GGAAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
 151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
 201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACTCGAGC
 251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
 301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
 351 TTCTATGTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
 401 TTAAAGCTAT TCCC GG TGAC CGGATTCTCA ATCAGTTCTG TATCGATTG
 451 GCTTCTTCGT CTAACCAAGG CGGGGGAGGA GATACTGATA CTACAAACAA
 501 GCGGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCACCACA GCGACGGCTG
 551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
 601 CTCGTTCACG CGCTTTGGC TTGGCCTGAA GCTGTTCAAGA AGGAGAATCT
 651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTTCTC
 701 AAATCGGAGC TATGAGAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGG
 751 CGGGGGATTT ACCGTCTCTC TCCGTCGCAG AGTCCAATCG ACCACTCTCT
 801 CTCCGATACT CTTTAGATGC ACTTCTACGA GACTTGTCT TATCTCAAGT
 851 TCGCTCACTT CACGGCGAAT CAAGGGATTC TCGAAGCTTT TCAAGGGAAAG
 901 AAAAGAGTTC ATGTCATTGA TTTCTCTATG AGTCAAGGGTC TTCAATGGCC
 951 GGCGCTTATG CAGGCTCTTG CCCITCGACC TGGTGGCTCT CCTGTTTCC
 1001 GGTTAACCGG AATTGGTCCA CGGGCACCGG ATAATTTCGA TTATCTTCAT
 1051 GAAGTTGGGT GAAAGCTGGC TCAATTAGCT GAGGGGATTC ACGTTGAGTT
 1101 TGAGTACAGA GGATTGTGG CTAACACTTT AGCTGATCTT GATGCTTCGA
 1151 TGCTTGAGCT TAGACCAAGT GAGATTGAAT CTGTTGGGGT TAACTCTGTT
 1201 TTGAGCTTC ACAAGCTCTT GGGACGACCT GGTGCGATCG ATAAGGTTCT
 1251 TGGTGTGGTG AATCAGATTA AACCGGAGAT TTTCACTGTC GTTGAGCAGG
 1301 AATCGAACCA TAATAGTCCG ATTTCCTTAG ATCGGTTTAC TGAGTCGTTG
 1351 CATTATTACT CGACGTTGTT TGACTCGTTG GAAGGTGTAC CGAGTGGTCA
 1401 AGACAAGGTC ATGTCGGAGG TTTACTTGGG TAAACAGATC TGCAACGTTG
 1451 TGGCTTGTGA TGGACCTGAC CGAGTTGAGC GTCATGAAAC GTTGAGTCAG
 1501 TGGAGGAACC GGTTCGGGTC TGCTGGGTTT GCGGCTGCAC ATATTGGTTC
 1551 GAATGCGTTT AAGCAAGCGA GTATGCTTTT GGCTCTGTTA AACGGCGGTG
 1601 AGGGTTATCG GGTGGAGGAG AGTGAACGGCT GTCTCATGTT GGG

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Figure 6(b)

1 MKRDHHHHHQ DKKTMMMNNEE DDGNGMDVAQ KLEQLEVMMMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTINKELK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRTYRLSPSQ SPIDHSLSDT L*

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Figure 6(c)

1 TAGAAGTGGT AGTGGACTGA AAAAAACAAAT CCTAAGCACT CCTAACCGAT
 51 CCCCCGAAGCT AAAGATTCTT CACCTTCCTA AATAAAGCAA AACCTAGATC
 101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
 151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
 201 GAATGAAGAA GACGGACGGTA ACGGCATGGA TGTTGCTCAG AAACCTCGAGC
 251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
 301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
 351 TTCTATGCTC ACCGACCTTA ATCCCTCCGTC GTCTAACGCC GAGTACGATC
 401 TTAAAGCTAT TCCCCTTGAC GCGATTCTCA ATCAGTTCGC TATCGATTG
 451 GCTTCTTCGT CTAACCAAGG CGGCAGGAGGA GATAACGTATA CTACAAACAA
 501 GCGGTTGAAA TGCTCAAACG CGCTCGTGG AACCACCCACA GCGACGGCTG
 551 AGTCAACTCG CCATGTTGTC CTGGTTGACT CGCAGGGAGAA CGGTGTTGCGT
 601 CTCGTTCAAG CGCTTTTGGC TTGCGCTGAA GCTGTTCTGA AGGAGAATCT
 651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTCTC
 701 AAATCGGAGC TATGAGAAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
 751 CGGCGGATTT ACCGTCTCTC TCCGTCGGAG AGTCCAATCG ACCACTCTCT
 801 CTCCGATACT CPTCAGATGC ACTTCTACGA GACTTGTCTT TATCTCAAGT
 851 TCGCTCACTT CACGGGAAT CAAGCGATTC TCGAAGCTTT TCAAGGGAAG
 901 AAAAGAGTTC ATGTCATTGA TTCTCTATGA GTCAAGGTCT TCAATGGCCG
 951 GCGCTTATGC AGGCTCTTGC GCTTCGACCT GGTGGTCTC CTGTTTTCCG
 1001 GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTTGAT TATCTTCATG
 1051 AAGTTGGGTG TAAGCTGGCT CATTAGCTG AGGGGATTCA CGTTGAGTTT
 1101 GAGTACAGAG GATTTGTGGC TAACACTTTA GCTGATCTT GATGCTTCGAT
 1151 GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTTGGGTT AACTCTGTTT
 1201 TCGAGCTTCA CAAGCTCTTGG GGACGACCTG GTGCGATCGA TAAGGTTCTT
 1251 GGTGTGGTGA ATCAGATTAA ACCGGAGATT TTCACTGTGG TTGAGCAGGA
 1301 ATCGAACCAT AATAGTCCGA TTTTCTTAA TCGGTTTACT GAGTCGTTGC
 1351 ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GACTGGTCAA
 1401 GACAAGGTCA TGTCGGAGGT TTACTTGTTT AAACAGATCT GCAACGTTGT
 1451 GGCTTGTGAT CGACCTGACC GACTTGAGCG TCATGAAACG TTGAGTCAGT
 1501 GGAGGAACCG GTTCGGGTCT CCTGGGTTTG CGGCTGCACA TATTGGTTCG
 1551 AATGCGTTTA ACCAAGCGAG TATGCTTTG GCTCTGTTCA ACGGCGGTCA
 1601 GGGTTATCGG GTGGAGGAGA GTGACGGCTG TCTCATCTTG GG

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Figure 6(d)

1 MKRDHHHHHQ DKKTMMMNNEE DDGNGMDVAQ KLEQLEVMMMS NVQEDDLSQL
51. ATETVHYNPA ELYTWLDSML TDLNPPSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTINKRLK CSNGVVETTT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQKENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT LQMHFYETCP YLKFAHFTAN QAIILEAFQGK
251 KRVHVIDS*

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Figure 6(e)

1 TAGAAGTGGT AGTCCAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
 51 CCCCCGAAGCT AAAGATTCTT CACCTTCCA AATAAAGCAA AACCTAGATC
 101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAA AAAACCAACC
 151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
 201 GAATGAAGAA GACCGACGGTA ACGGCATGGA TGTTGCTCAG AAACTCGAGC
 251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
 301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CCTGGCTTGA
 351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
 401 TTAAAGCTAT TCCCGGTGAC GCGATTCTCA ATCAGTTGCG TATCGATTG
 451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACGTATA CTACAAACAA
 501 GCGGTTGAAA TGCTCAAACG GCGTCGTGGA AACCAACCACA GCGACGGCTG
 551 AGTCAACTCG GCATGTTGTC CTGGTTGACT CGCAGGAGAA CGGTGTGCGT
 601 CTCGTTCACG CGCTTTGGC TTGCGCTGAA GCTGTTCAGA AGGAGAATCT
 651 GACTGTGGCG GAAGCTCTGG TGAAGCAAAT CGGATTCTTA GCTGTTCTC
 701 AAATCGGAGC TATGAGAAA GTCGCTACTT ACTTCGCCGA AGCTCTCGCG
 751 CGGCGGATTT ACCGTCTCTC TCCGTCGCAG AGTCCAATCG ACCACTCTCT
 801 CTCCGATACT CTTCAGATGC ACTTCTACGA GACTTGTCTT TATCTCAAGT
 851 TCGCTCACTT CACGGCGAAT CAAGCGATTIC TCGAAGCTTT TCAAGGGAAAG
 901 AAAAGAGTTC ATGTCATTGA TTTCTCTATG AGTCAAGGTC TTGGGGCGTT
 951 ATGCAGGCTC TTGCGCTTCG ACCTGGTGGT CCTCCTGTT TCCGGTTAAC
 1001 CGGAATTGGT CCACCGGCAC CGGATAATTT CGATTATCTT CATGAAGTTG
 1051 GGTGTAAGCT GGCTCATTAA GCTGAGGGCA TTACCGTTGA GTTTGAGTAC
 1101 AGAGGATTG TGGCTAACAC TTTAGCTGAT CTTGATGCTT CGATGCTTGA
 1151 GCTTAGACCA AGTGAGATTG AATCTGTTGC GGTAACTCT GTTTTCGAGC
 1201 TTCACAAGCT CTTGGGACGA CCTGGTGCAG TCGATAAGGT TCTTGGTGTG
 1251 GTGAATCAGA TTAAACCGGA GATTTCACT GTGGTTGAGC AGGAATCGAA
 1301 CCATAATAGT CCGATTTCT TAGATCGGTT TACTGAGTCG TTGCATTATT
 1351 ACTCGACGTT GTTGACTCG TTGGAAGGTG TACCGAGTGG TCAAGACAAAG
 1401 GTCATGTCGG AGGTTTACTT GGGTAAACAG ATCTGCAACG TTGTGGCTTG
 1451 TGATGGACCT GACCGAGTTG AGCGTCATGA AACGTTGAGT CAGTCGACCGA
 1501 ACCGGTTCGG GTCTGCTGGG TTTGCGGCTG CACATATTGG TTCAATGCG
 1551 TTTAAGCAAG CGAGTATGCT TTTGGCTCTG TTCAACGGCG GTGAGGGTTA
 1601 TCGGGCTGGAG GACAGTGACCG GCTGTCTCAT GTTGGG

Figure 6(f)

1 MKRHHHHHQ DKKTMMNEE DDGNGMDVAQ KLEQLEVMMMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTNKRLK CSNGVVEETT ATAESTRHVV LVDSQENGVR
151 LVHALLACAE AVQXENLTVA EALVKQIGFL AVSQIGAMRK VATYFAEALA
201 RRIYRLSPSQ SPIDHSLSDT LQMHFYETCP YLKFAHFTAN QAILLEAFQCK
251 KRVAVIDFSM SQGLGRLCRL LRFDLVVLIF SG*

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Figure 6(g)

1 TAGAACTGGT AGTGGAGTGA AAAAACAAAT CCTAAGCAGT CCTAACCGAT
 51 CCCCCGAAGCT AAAGATTCTT CACCTTCCCA AATAAAGCAA AACCTAGATC
 101 CGACATTGAA GGAAAAACCT TTTAGATCCA TCTCTGAAAA AAAACCAACC
 151 ATGAAGAGAG ATCATCATCA TCATCATCAA GATAAGAAGA CTATGATGAT
 201 GAATGAAGAA GACGACGGTA ACGGCATGGA TGTTGCTCAG AAACTCGAGC
 251 AGCTTGAAGT TATGATGTCT AATGTTCAAG AAGACGATCT TTCTCAACTC
 301 GCTACTGAGA CTGTTCACTA TAATCCGGCG GAGCTTTACA CGTGGCTTGA
 351 TTCTATGCTC ACCGACCTTA ATCCTCCGTC GTCTAACGCC GAGTACGATC
 401 TTAAAGCTAT TCCCAGTGAC GCGATTCCTCA ATCAGTTTCGC TATCGATTG
 451 GCTTCTTCGT CTAACCAAGG CGGCGGAGGA GATACTGATA CTACAAACAA
 501 GCGGGTGAAGA TGCTAAACG GCGTCGTGGA AACCACCAACA GCGACGGCTG
 551 AGTCAACTCG GCATGTGTCC TGGTTGACTC GCAGGAGAAC GGTGTGCGTC
 601 TCGTTCACGC GCTTTGGCT TGCGCTGAAG CTGTTCAGAA GGAGAATCTG
 651 ACTGTGGCGG AAGCTCTGGT GAAGCAAATC GGATTCTTAG CTGTTCTCA
 701 AATCGGAGCT ATGAGAAAAG TCGCTACTTA CTTCGCCGAA GCTCTCGCGC
 751 GGCAGGATTAA CCGTCTCTCT CCAGTCGAGA GTCCAATCGA CCACTCTCTC
 801 TCCGATACTC TTCAGATGCA CTTCTACGAG ACTTGTCCCTT ATCTCAAGTT
 851 CGCTCACTTC ACAGGCGAAC AAGCGATTCT CGAAGCTTT CAAGGGAAGA
 901 AAAGAGTTCA TGTCAATTGAT TTCTCTATGA GTCAAGGTCT TCAATGGCCG
 951 GCGCTTATGC AGGCTCTTGC GCTTCGACCT GGTGGTCCTC CTGTTTCCG
 1001 GTTAACCGGA ATTGGTCCAC CGGCACCGGA TAATTTCGAT TATCTTCATG
 1051 AAGTTGGGTG TAAGCTGGCT CATTAGCTG AGGCGATTCA CGTTGAGTTT
 1101 GAGTACAGAG GATTTGTGGC TAACACTTTA GCTGATCTTG ATGCTTCGAT
 1151 GCTTGAGCTT AGACCAAGTG AGATTGAATC TGTTGGGGTT AACTCTGTTT
 1201 TCGAGCTTCA CAAGCTCTTG GGACGGACCTG GTGGATCGA TAAGGTTCTT
 1251 GGTGTGGTGA ATCAGATTAA ACCGGAGATT TTCACTGTGG TTGAGCAGGA
 1301 ATCGAACCAT AATAGTCCGA TTTTCTTAGA TCGGTTTACT GAGTCGTTGC
 1351 ATTATTACTC GACGTTGTTT GACTCGTTGG AAGGTGTACC GAGTGGTCAA
 1401 GACAAGGTCA TGTCGGAGGT TTACTTGGGT AAACAGATCT GCAACGTTGT
 1451 GGCTTGTGAT GGACCTGACC GAGTTGAGCG TCATGAAACG TTGAGTCAGT
 1501 GGAGGAACCG GTTCGGGTTCT GCTGGGTTG CGGCTGCACA TATTGGTTCG
 1551 AATGGGTTTA AGCAAGCGAG TATGTTTGTG GCTCTGTTCA ACGGGCGGTGA
 1601 GCGTTATCGG GTGGAGGAGA GTGACGGCTG TCTCATGTTG GG

Figure 6(h)

1 MKRDHHHHHQ DKKTMMNEE DDGNGMDVAQ KLEQLEVMS NVQEDDLSQL
51 ATETVHYNPA ELYTWLDSML TDLNPPSSNA EYDLKAIPGD AILNQFAIDS
101 ASSSNQGGGG DTYTTINKRLK CSNGVVETTT ATAESTRHVS WLTRRRRTVCV
151 SFTRFWLALK LFRRRI*